

Application of SIR epidemiological model: new trends*

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Abstract

The simplest epidemiologic model composed by mutually exclusive compartments SIR (susceptible-infected-susceptible) is presented to describe a reality. From health concerns to situations related with marketing, informatics or even sociology, several are the fields that are using this epidemiological model as a first approach to better understand a situation. In this paper, the basic transmission model is analyzed, as well as simple tools that allows us to extract a great deal of information about possible solutions. A set of applications - traditional and new ones - is described to show the importance of this model.

Keywords: SIR, epidemiological models, basic reproduction number, differential equations, applications.

1 Introduction

Epidemiology has become an important issue for modern society. The relationship between mathematics and epidemiology has been increasing. For the mathematician, epidemiology provides new and exciting branches, while for the epidemiologist, mathematical modeling offers an important research tool in the study of the evolution of diseases.

The SIR model, developed by Ronald Ross, William Hamer, and others in the early twentieth century [2], consists of a system of three coupled nonlinear ordinary differential equations.

Theoretical papers by Kermack and McKendrick, between 1927 and 1933 about infectious disease models, have had a great influence in the development of mathematical epidemiology models [32]. Most of the basic theory had been developed during that time, but the theoretical progress has been steady since then [5]. Mathematical models are being increasingly used to elucidate the transmission of several diseases. These models, usually based on compartment models, may be rather simple, but studying them is crucial in gaining important knowledge of the underlying aspects of the infectious diseases spread out [16], and to evaluate the potential impact of control programs in reducing morbidity and mortality.

Recent years have seen an increasing trend in the representation of mathematical models in publications in the epidemiological literature, from specialist journals of medicine, biology and mathematics to the highest impact generalist journals [11], showing the importance of interdisciplinary.

But this epidemiological model crossed the borders of health and biology. In several fields, the concept of spreading is applied and, a pragmatic point of view, the SIR model is a beginning point

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to understand what happens rapidly; then, with more understanding and complexity is possible to enrich the model and put more details in the formulation.

The paper is organized as follows. Next section the SIR model is presented, as well as some theoretical results that allows to understand the transmission process. Then a set of application from distinct fields are exposed in Section 3 and, finally, some concluding remarks are done.

2 SIR model

Mathematical models are a simplified representation of how an infection spreads across a population over time.

Most epidemic models are based on dividing the population into a small number of compartments. Each containing individuals that are identical in terms of their status with respect to the disease in question. In the SIR model, the three compartments are:

- *Susceptible* (S): is the class of individuals who are susceptible to infection; this can include the passively immune once they lose their immunity or, more commonly, any newborn infant whose mother has never been infected and therefore has not passed on any immunity;
- *Infected* (I): in this class, the level of parasite is sufficiently large within the host and there is potential in transmitting the infection to other susceptible individuals;
- *Recovered or Resistant* (R): includes all individuals who have been infected and have recovered.

This epidemiological model captures the dynamics of acute infections that confers lifelong immunity once recovered. Diseases where individuals acquire permanent immunity, and for which this model may be applied, include measles, smallpox, chickenpox, mumps, typhoid fever and diphtheria.

Generally, the total population size is considered constant, *i.e.*, $N = S + I + R$. Then two cases should be studied, distinguished by the inclusion or exclusion of demographic factors.

2.1 The SIR model without demography

Having compartmentalized the population, we now need a set of equations that specify how the sizes of compartments change over time.

The SIR model, excluding births and deaths, can be defined as

$$\begin{aligned}\frac{dS}{dt} &= -\beta SI \\ \frac{dI}{dt} &= \beta SI - \gamma I \\ \frac{dR}{dt} &= \gamma I\end{aligned}\tag{1}$$

subject to initial conditions $S(0) > 0$, $I(0) \geq 0$ and $R(0) \geq 0$.

In addition, the transmission rate, per capita, is β and the recovery rate is γ .

There are three commonly used threshold values in epidemiology: \mathcal{R}_0 , σ and R . The most common and probably the most important is the basic reproduction number [15, 17, 18]. The basic reproduction number, denoted by \mathcal{R}_0 , is defined as the average number of secondary infections that occurs when one infective is introduced into a completely susceptible population.

This threshold, \mathcal{R}_0 , is a famous result due to Kermack and McKendrick [24] and is referred to as the “threshold phenomenon”, giving a borderline between a persistence or a disease death. \mathcal{R}_0 it is also called the basic reproduction ratio or basic reproductive rate.

The contact number, σ is the average number of adequate contacts of a typical infective during the infectious period.

An adequate contact is one that is sufficient for transmission, if the individual contacted by the susceptible is an infective. It is implicitly assumed that the infected outsider is in the host population for the entire infectious period and mixes with the host population in exactly the same way that a population native would mix.

The replacement number, R , is the average number of secondary infections produced by a typical infective during the entire period of infectiousness.

Note that the replacement number R changes as a function of time t as the disease evolves after the initial invasion.

These three quantities \mathcal{R}_0 , σ and R are all equal at the beginning of the spreading of an infectious disease when the entire population (except the infective invader) is susceptible. \mathcal{R}_0 is only defined at the time of invasion, whereas σ and R are defined at all times.

The replacement number R is the actual number of secondary cases from a typical infective, so that after the infection has invaded a population and everyone is no longer susceptible, R is always less than the basic reproduction number \mathcal{R}_0 . Also after the invasion, the susceptible fraction is less than one, and as such not all adequate contacts result in a new case. Thus the replacement number R is always less than the contact number σ after the invasion [17]. Combining these results leads to

$$\mathcal{R}_0 \geq \sigma \geq R.$$

Note that $\mathcal{R}_0 = \sigma$ for most models, and $\sigma > R$ after the invasion for all models.

For the models throughout this study the basic reproduction number, \mathcal{R}_0 , will be applied. When

$$\mathcal{R}_0 < 1$$

the disease cannot invade the population and the infection will die out over a period of time. The amount of time this will take generally depends on how small \mathcal{R}_0 is. When

$$\mathcal{R}_0 > 1$$

invasion is possible and infection can spread through the population. Generally, the larger the value of \mathcal{R}_0 the more severe, and possibly widespread, the epidemic will be [10].

In this SIR model, when a newly introduced infected individual can be expected to infect other people at the rate β during the expected infectious period $1/\gamma$. Thus, this first infective individual can be expected to infect

$$\mathcal{R}_0 = \frac{\beta}{\gamma}.$$

2.2 The SIR model with demography

The simplest and most common way of introducing demography into the SIR model is to assume there is a natural host lifespan, $1/\mu$ years. Then, the rate at which individuals, at any epidemiological compartment, suffer natural mortality is given by μ . It is important to emphasize that this factor is independent of the disease and is not intended to reflect the pathogenicity of the infectious agent. Historically, it has been assumed that μ also represents the population's crude birth rate, thus ensuring that total population size does not change through time, or in other words, $\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0$.

So, the SIR model, including births and deaths, can be defined as

$$\begin{aligned}\frac{dS}{dt} &= \mu - \beta SI - \mu S \\ \frac{dI}{dt} &= \beta SI - \gamma I - \mu I \\ \frac{dR}{dt} &= \gamma I - \mu R\end{aligned}\tag{2}$$

with initial conditions $S(0) > 0$, $I(0) \geq 0$ and $R(0) \geq 0$.

It is important to introduce the \mathcal{R}_0 expression for this model. The parameter β represents the transmission rate per infective and the negative terms in the equation tell us that each individual spends an average $\frac{1}{\gamma+\mu}$ time units in this class. Therefore, if we assume the entire population is susceptible, then the average number of new infectious per infectious individual is determined by

$$\mathcal{R}_0 = \frac{\beta}{\gamma + \mu}.$$

The inclusion of demographic dynamics may allow a disease to die out or persist in a population in the long term. For this reason it is important to explore what happens when the system is at equilibrium.

A model defined SIR has an equilibrium point, if a triple $E^* = (S^*, I^*, R^*)$ satisfies the following system:

$$\begin{cases} \frac{dS}{dt} = 0 \\ \frac{dI}{dt} = 0 \\ \frac{dR}{dt} = 0 \end{cases}.$$

If the equilibrium point has the infectious component equal to zero ($I^* = 0$), this means that the pathogen suffered extinction and E^* is called Disease Free equilibrium (DFE).

If $I^* > 0$ the disease persist in the population and E^* is called Endemic Equilibrium (EE).

With some calculations and algebraic manipulations, it is possible to obtain two equilibria for the system (2):

$$\begin{aligned} \text{DFE: } E_1^* &= (1, 0, 0) \\ \text{EE: } E_2^* &= \left(\frac{1}{\mathcal{R}_0}, \frac{\mu}{\beta} (\mathcal{R}_0 - 1), 1 - \frac{1}{\mathcal{R}_0} - \frac{\mu}{\beta} (\mathcal{R}_0 - 1) \right) \end{aligned}$$

When $\mathcal{R}_0 < 1$, each infected individual produces, on average, less than one new infected individual, and therefore, predictable that the infection will be cleared from the population. If $\mathcal{R}_0 > 1$, the pathogen is able to invade the susceptible population [15, 17]. It is possible to prove that for the Endemic Equilibrium to be stable, \mathcal{R}_0 must be greater than one, otherwise the Disease Free Equilibrium is stable. More detailed information about local and global stability of the equilibrium point can be found in [7, 20, 27, 30].

This threshold behavior is very useful, once we can determine which control measures, and at what magnitude, would be most effective in reducing \mathcal{R}_0 below one, providing important guidance for public health initiatives.

Next section some applications of this epidemiological model are presented, as well as a set of references that can complement the information given.

3 Applications

3.1 Health

3.1.1 Influenza

Consider an epidemic of influenza in a British boarding school [23]. Three boys were reported to the school infirmary with the typical symptoms of influenza. Over the next few days, a very large fraction of the 763 boys in the school had contact with the infection. Within two weeks, the infection had become extinguished. The best fit parameters yield an estimated active infectious period of $1/\gamma = 2.2$ days and a mean transmission rate $\beta = 1.66$ per day. Therefore, the estimated \mathcal{R}_0 is 3.652. Figure 1 represents the dynamics of the three state variables. It can be observed that the curve of susceptible is decreasing all over the time, because the birth was no considered, and once become infected never returns to the state of susceptible. The curve of infected reaches to a peak of the disease beyond 5 weeks. This information could be very useful for health authorities to ensure that all resources are available - medicines, doctors, hospitalization resources - to provide a

good health care if necessary. Depending of flatness of the curve the response should be adaptive. The curve related to the recovered compartment is important because accumulates the number of individuals that have been seek in that outbreak.

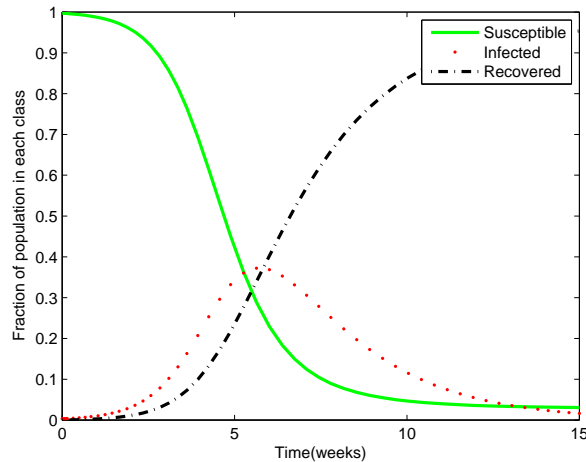


Figure 1: The time-evolution of influenza over 15 days

More information about this disease and other authors that studied influenza can be found in [19, 22, 34].

In other examples the curves do not be shown, instead the only thing that are changed are the parameters values. The main goal of this paper is not to show all the graphics related to SIR model, but to present a set of applications in several fields.

3.1.2 Dengue Fever

Dengue is a vector-borne disease transmitted from an infected human to a female *Aedes* mosquito by a bite. Then, the mosquito, that needs regular meals of blood to feed their eggs, bites a potential healthy human and transmits the disease making it a cycle. Nowadays, Dengue is the mosquito-borne infection that has become a major international public health concern. According to the World Health Organization (WHO), 50 to 100 million Dengue Fever infections occur yearly, including 500000 Dengue Hemorrhagic Fever cases and 22000 deaths, mostly among children [43].

This global pandemic is attributed to the unprecedented population growth, the rising level of urbanization without adequate domestic water supplies, increasing movement of the virus between humans (due to tourism, migration, or international trade), and lack of effective mosquito control. Dengue virus is transmitted to humans through the bite of infected *Aedes* mosquitoes, specially *Aedes Aegypti*. Once infected, a mosquito remains infected for life, transmitting the virus to susceptible individuals during feed. Without a vaccine, vector control remains the only available strategy against dengue. Appropriate mathematical models can give a deeper insight into the mechanism of disease transmission.

In this particular disease, the SIR model associated to the human population, usually is coupled to a SI model for the mosquito, due to the vector transmission process. More details, can be found in [37]-[40].

3.1.3 SARS

The Severe Acute Respiratory Syndrome (SARS) was the first epidemic of the 21st century. It emerged in China late 2002 and quickly spread to 32 countries causing more than 774 deaths and 8098 infections worldwide [33].

SARS is a highly contagious respiratory disease which is caused by the SARS Coronavirus. It is a serious form of pneumonia, resulting in acute respiratory distress and sometimes death. The SARS epidemic originated in China, in late 2002. Although the Chinese government tried to control the outbreak of the SARS epidemic without the awareness of the World Health Organization (WHO), it continued to spread.

In the research papers [29] and [41] they use the SIR model, as a first approach to explain this disease. They use the super-spreading individuals - infected individuals that infect more than the average number of secondary cases - to modify the traditional epidemiological model. The effect of super-spreaders can be used in cases where there is a higher transmission rate.

3.2 Networks

3.2.1 Online social networks

The last decade has seen a huge number of online social networks (such as Facebook, Twitter, MySpace, Instagram, LinkedIn,...). Several papers have studied, under epidemiological models, the adoption or abandonment of online social networks. Cannarella and Spechler [6] studied the information diffusion on Twitter, in order to understand the properties of underlying media and model communication patterns; with the popularity of Twitter it became a venue to broadcast rumors and misinformation.

Wang and Wang [42] investigate a SIR model to study rumor spreading. With the development of microblogging technology, it became easy to publish several messages on the network websites, and also for other people to be able to visit these websites to search for messages according to their own needs, increasing rapidly the social network.

3.2.2 Viral Marketing

Viral marketing (VM) is a recent approach to markets and can potentially reach a large and fast audience, through a cheap communication campaign. VM exploits existing social networks by encouraging people to share product information and campaigns with their friends, through email or networks medium. This type of communication has more impact on the customer, because the information was recommended by friends and peer networks that know the personal interests, instead of standard companies; this kind of communication has more impact because it is directly targeted. Besides, when a marketing message goes viral, it is analogous to an epidemic, since it involves a person-to-person transmission, spreading within a population. Rodrigues and Fonseca [36] explored a set of simulation experiments to explore the influence of several controlled and external factors that could influence viral campaigns.

Also known as internet word of mouth marketing, VM has been gaining more fans, from professionals to researchers, as an alternative strategy to traditional communication, transferring funds from companies to online marketing actions and exploring this spreading phenomenon [21, 35].

3.2.3 Audience applause

The social identity and crowd psychology study how and why an individual changes their behavior in response to others; within a group, a distinct attitude can arise in a few persons and then spread quickly to all other members.

According to Mann *et al.* [28] individuals' probability of starting clapping increased in proportion to the number of other audience members already affected by this social contagion. In this paper, the authors apply a Bayesian model selection approach to determine the dynamics of how some details or social cues can provoke the spread of social behavior in a group of people. They reach the conclusion that the audience clapping can vary, even when the quality of the presentations are identical, changing according to the set of infected people.

3.2.4 Diffusion of ideas

The population dynamics underlying the diffusion of ideas hold many qualitative similarities to those involved in the spread of infections. Bettencourt *et al.* [4] explore this point of view as a tool to quantify sociological and behavioral patterns. They explore the spreading of Feynman diagram through the theoretical physics communities of the USA, Japan, and the USSR in the period immediately after World War II; having this in mind they investigate the effectiveness of the adoption of an idea, finding values for parameters that describe intentional social organization and long lifetimes for the idea.

By other hand, Funk [12], explore the concept of epidemiology in the human behavior when public campaigns and mass media reports are diffused. The spread of awareness is crucial in this model to describe the susceptible person to become convinced or informed to the disease and have additional precautions related to the disease transmission process.

3.3 Informatics

3.3.1 Peer-to-peer (P2P) newtworks

Understanding the spread of information on complex networks is crucial from a theoretical and applied perspective. To evaluate them with large-scale real-world data remains an important challenge.

During the downloading process, the peer shares the downloaded parts of the file and, thus, contributes to distributing it in the network [26]. The authors consider a file sharing application similar to eDonkey which belongs to the class of hybrid P2P architectures and apply the SIR model, that corresponds to the populations of idle peers, peers currently downloading the file, and those sharing it.

Bernardes *et al.* [3] asses the relevance of the SIR model to mimic key properties of spreading cascade of a file sharing.

3.3.2 Spread of computer virus

Nowadays, with the rapid development of network information technology, information networks security has become a very critical issue in our work and daily life. The computer virus are being developed simultaneously with the computer systems and the use of internet facilities increases the number of damaging virus incidents, producing serious problems for individuals and corporate computer systems. Antivirus software is the major means of defending against viruses. Although, antivirus technique cannot predict the evolution trend of viruses and, hence, cannot provide global suggestions for their prevention and control. The strong desire to understand the spread mechanism of computer viruses has motivated the proposal of a variety of epidemic models that are based on fully connected networks, that is, networks where each computer is equally likely to be accessed by any other computer.

Computer virus is considered as one of the most important weapon in the internet, and their emergence and spread may have great effect on the computer world. Different codes have different ways to spread in the internet. Virus mainly attack the file system and worm uses system vulnerability to search and attack the computer. And for trojan horses, they camouflage themselves and thus induce the users to download them. There are a variety of computer virus, but they all have infectivity, invisibility, latent, destructibility and unpredictability [7]. The word latent means that the virus hide themselves in the computer and spread them in the internet while the users can not notice them. More details about applications to the spread of computer virus can be found in [9, 13, 14, 44].

3.4 Economics and Finance

3.4.1 Rational expectations

The economic epidemiology merges the epidemiological models with economic choice, translating a rational decision making. Economic research in this area began in response to the AIDS epidemic and has led to an improved understanding of the thought/decisions towards a infectious disease, by anonymous individuals or policymakers [1]. the power to eradicate an infectious disease is not only in the hands of policymakers or health authorities: it is also important that rational individuals made their own response to lower the prevalence of a disease, by increasing protection. Economic epidemiology has made significant advances in educating health officials about the behavioral implications of public policies. Aadland *et al.* explored the nature of the short-run equilibrium dynamics for rational expectations economic epidemiological systems. They show that well-intentioned policy has the potential to create instability when people behave rationally and in a self-interested manner.

3.4.2 Financial network contagion

The financial sector is always a theme of interest, due to its importance in economy in general, and our daily lives in particular. Some papers [?, ?] analyze the importance of individual bank-specific factors on financial stability. The spreading of the contagion in the interbank network can be seen as an epidemiological model. The authors investigate the systemic risk and how this risk can propagate in different bank and countries within the euro area. Fisher makes counterfactual simulations to propagate shocks emerging from three sources of systemic risk: interbank, asset price, and sovereign credit risk markets. when the conditions deteriorate, these channels trigger severe direct and indirect losses and cascades of defaults, whilst the dominance of the sovereign credit risk channel amplifies, as the primary source of financial contagion in the banking network.

3.5 Science Fiction: Zombies attack

In 2009, the first mathematical investigation of the zombie community appears. Taking their cues from traditional zombie movies, Munz *et al.* [31] hypothesized the effect of a zombie attack and its impact on human civilization. According to their mathematical model, “a zombie outbreak is likely to lead to the collapse of civilization, unless it is dealt with quickly. While aggressive quarantine may contain the epidemic, or a cure may lead to coexistence of humans and zombies, the most effective way to contain the rise of the undead is to hit hard and hit often.” The model showed two equilibria: the disease-free equilibrium (with no zombies) and the doomsday equilibrium (where everyone is a zombie). The application of a linear stability analysis showed that - in the absence of further interventions - the disease-free equilibrium was unstable and the doomsday equilibrium was stable. Since this paper, other authors follow this area with a careful attention (see more in [8, 25]), not only motivated by the tv series, but as a way to motivate young students for the epidemiology issues.

4 Conclusion

Deterministic models applied to the study of infectious disease have a long tradition. The importance to predict the evolution of a disease, its impact in population and in the health systems - human and material resources - has a long concern to human population. However, with the increasing of new technologies and the growth of the interdisciplinarity, new researchers are become interested in epidemiological models to apply in other fields.

In this paper a selection of application from different fields was presented where the SIR models was used. This exposition is not exhaustive, but is a selection of recent areas that are been developed and where the epidemiological mathematics is a possible response to describe reality.

Networks and the epidemiology of directly transmitted infectious diseases are fundamentally linked. Most of the themes that involve the diffusion phenomena could start to simulate and understand some scenarios with simple epidemiological models. They can be seen as a first tool to try when a new problem presents itself, due to its limitations. But as simple as they seem, they are a huge help to define new step in research and an emergency response to a crisis when time to predict is short.

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References

- [1] D. Aadland, D. Finnoff and K. Huang, The dynamics of economic epidemiology equilibria. *Working Paper*, 2011.
- [2] R. M. Anderson, Discussion: the Kermack-McKendrick epidemic threshold theorem. *Bulletin of mathematical biology*, 53(1): 1–32, 1991.
- [3] D. F. Bernardes, M. Latapy and F. Tarissan, Relevance of SIR model for Real-World spreading phenomena: experiments on large-scale P2P system. *IEEE/ACM International Conference on Advances in Social Networks Analysis and Mining*, 327–334, 2012.
- [4] L. M. A. Bettencourt, A. Cintrn-Arias, D. I. Kaiser and C. Castillo-Chvez, The power of a good idea: quantitative modeling of the spread of ideas from epidemiological models. *Physica A*, 364: 513–536, 2006.
- [5] F. Brauer, Compartmental models in epidemiology, in *Mathematical epidemiology*, vol. 1945, Berlin: Springer, 19–79, 2008.
- [6] J. Cannarella and J. A. Spechler, *Epidemiological modeling of online social network dynamics*, (preprint).
- [7] C. Castillo-Chavez, Z. Feng and W. Huang, On the computation of R_0 and its role in global stability. in *Mathematical Approaches for Emerging and Reemerging Infectious Diseases: An Introduction*, 125, Springer, 229–250, 2002.
- [8]
- [9] C. Deng and Q. Liu, A computer virus spreading model with nonlinear infectivity on scale-free network, in *International Conference on Information Sciences, Machinery, Materials and Energy*. Atlantis Press, 1684–1688, 2012.
- [10] P. van den Driessche and J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Math. Biosci.*, 180: 29–48, 2002.
- [11] N. M. Ferguson, D. A. T. Cummings, C. Fraser, J. C. Cajka, P. C. Cooley and D. S. Burke, Strategies for mitigating an influenza pandemic. *Nature*, 442, 448–452, 2006.
- [12] S. Funk and V. Jansen, The Talk of the Town: Modelling the Spread of Information and Changes in Behaviour. in *Modeling the Interplay Between Human Behavior and the Spread of Infectious Diseases* New York: Springer New York, 93–102, 2012

- [13] C. Gan, X. Yang, W. Liu, Q. Zhu and X. Zhang, Propagation of computer virus under human intervention: a dynamical model. *Discrete Dynamics in Nature and Society*, Hindawi Publishing Corporation ID106950, 2012.
- [14] X. Han and Q. Tan, Dynamical behavior of computer virus on Internet. *Applied Mathematics and Computation*, 217: 2520–2526, 2010.
- [15] J. R. Heffernan, R. J. Smith and L. M. Wahl, Perspective on the basic reproductive ratio. *J. R. Soc. Interface*, 2: 281–293, 2005.
- [16] H. W. Hethcote, A Thousand and One Epidemic Models. *Frontiers in Theoretical Biology*, 100: 504–515, 1994.
- [17] H. W. Hethcote, The mathematics of infectious diseases. *SIAM Rev.*, 42(4): 599–653, 2000.
- [18] H. W. Hethcote, The basic epidemiology models: models, expressions for R_0 , parameter estimation, and applications, in *Mathematical Understanding of Infectious Disease Dynamics*, Lecture Notes Series Institute for Mathematical Sciences, National University of Singapore, 1–61, 2008.
- [19] M. B. Hooten, J. Anderson and L. A. Waller. Assessing North American influenza dynamics with a statical SIRS model. *Spatial and Spatio-temporal Epidemiology*, 1: 177–185, 2010.
- [20] J. C. Kamgang and G. Sallet, Computation of threshold conditions for epidemiological models and global stability of the disease-free equilibrium (DFE). *Mathematical Biosciences*, 213: 1–12, 2008.
- [21] K. Kandhaway and J. Kuri, How to run a campaign: optimal control of SIS and SIR information epidemics. *Applied Mathematics and Computation*, 231: 79–92, 2014.
- [22] S. A. A. Karim and R. Razali, A Proposed Mathematical Model of Influenza A, H1N1 for Malaysia. *Journal of Applied Sciences*, 11: 1457–1460, 2011.
- [23] M. J. Keeling and P. Rohani, *Modeling infectious diseases in humans and animals*, Princeton, NJ: Princeton University Press. xiii, 2008.
- [24] W. O. Kermack and A. G. McKendrick, A contribution to the mathematical theory of epidemics. *Proceedings Royal Soc. London (A)*, 115: 700–721, 1927.
- [25] H. P. Langtangen, K.-A. Mardal and P. Røtnes, Escaping the zombie threat by mathematics. In: *Zombies in the Academy - Living Death in Higher Education* Chicago: University of Chicago Press, 2013.
- [26] K. Leibnitz, T. Hossfeld, N. Wakamiya and M. Murata Modeling of epidemic diffusion in peer-to-peer file-sharing networks *Biologically Inspired Approaches to Advanced Information Technology*, LNCS, vol. 3853, Springer Verlag, 322–329, 2006.
- [27] M. Y. Li and J. S. Muldowney, A geometric approach to global-stability problems. *SIAM J. Math. Anal.*, 27(4): 1070–1083, 1996.
- [28] R. P. Mann, J. Faria, D. J. T. Sumpter and J. Krause, The dynamics of audience applause. *Journal of the Royal Society Interface*, 10:20130466.
- [29] T. Mkhathshwa2011 and A. Mummert, Modeling Super-spreading Events for Infectious Diseases: case study SARS. *IAENG International Journal of Applied Mathematics*, 41:2, 2011.
- [30] J. S. Muldowney, M. Y. Li, M. Y. and P. van den Driessche, Global stability of SEIR models in epidemiology. *Can. Appl. Math. Quart.*, 7: 155–164, 1999.

- [31] P. Munz, I. Hudea, J. Imad and R. Smith, When zombies attack!: Mathematical modelling of an outbreak of zombie infection. In: *Tchuenche, J.M., Chiyaka, C. (eds.) Infectious Disease Modelling Research Progress* Nova Science Publishers, 133–150, 2009.
- [32] J. D. Murray, *Mathematical Biology* New York: Springer-Verlag, 2002.
- [33] T. W. Ng, G. Turinici and A. Danchin, A double epidemic model for the SARS propagation, *BMC Infectious Diseases*, 3:19, 2003.
- [34] K. L. Nichol, K. Tummers, A. Hoyer-Leitzel, J. Marsh, M. Moynihan and S. McKelvey, Modeling Seasonal Influenza Outbreak in a Closed College Campus: Impact of Pre-Season Vaccination, In-Season Vaccination and Holidays/Breaks. *PLoS ONE* 5(3): e9548. doi: 10.1371/journal.pone.0009548
- [35] H. S. Rodrigues and M. J. Fonseca, Viral Marketing as epidemiological model. *Proceedings of the 15th International Conference on Computational and Mathematics Methods in Science and Engineering* 946–955, 2015.
- [36] H. S. Rodrigues and M. J. Fonseca, Can information be spread as a virus? Viral Marketing as epidemiological model. *Mathematical Methods in the Applied Sciences*, (in press).
- [37] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres, Optimization of Dengue epidemics: a test case with different discretization schemes, in *Numerical analysis and applied mathematics. International conference on numerical analysis and applied mathematics, Crete, Greece. American Institute of Physics Conf. Proc.*, 1168: 1385–1388, 2009.
- [38] H. S. Rodrigues, M. T. T. Monteiro, D. F. M. Torres and A. Zinober Dengue disease, basic reproduction number and control, *Int. J. Comput. Math.*, 89(3): 334–346, 2012.
- [39] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres, Dengue in Cape Verde: vector control and vaccination, *Math. Population Studies*, 20(4): 208–223, 2013.
- [40] H. S. Rodrigues, M. T. T. Monteiro and D. F. M. Torres, Dengue in Cape Verde: vector control and vaccination, in *In Dynamics, Games and Science - International Conference and Advanced School Planet Earth DGS II. Bourguignon et al. (Eds). Springer International Publishing Switzerland*, 593–605, 2015.
- [41] M. Small, P. Shi and C. K. Tse, Plausible Models for Propagation of the SARS Virus, *IEICE Trans. Fundamentals*, e87-A(9): 2379–2386, 2004.
- [42] J. Wang and Y.-Q. Wang, SIR Rumor Spreading Model with Network Medium in Complex Social Networks, *Chinese Journal of Physics*, 53(1): 020702, 2015.
- [43] WHO. *Dengue: guidelines for diagnosis, treatment, prevention and control*. World Health Organization, 2nd edition, 2009.
- [44] Q. Zhu, X. Yang and J. Ren, Modeling and analysis of the spread of computer virus. *Commun nonlinear Sci Numer Simulat*, 17: 5117–5124, 2012.